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MAEQLH (TM)

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 23 10:08:31 1999; MasPar time 4.19 Seconds  
78.109 Million cell updates/sec

Tabular output not generated.

Title: >US-09-177-843-1  
Description: (1-6) from US09177843.pep  
Perfect Score: 41  
Sequence: 1 GRGDSP 6

Scoring table: PAM 150  
Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sptrmb19

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle  
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified  
13:sp-vertebrate 14:sp-virus

Statistics: Mean 18.281; Variance 16.870; scale 1.084

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
1	41	100.0	1095	099458	NOTCH4 (FRAGMENT).	2.18e+00
2	41	100.0	2478	093406	FIBRONECTIN.	2.18e+00
3	40	97.6	95	050799	COBALT TRANSPORT PROTE	4.11e+00
4	40	97.6	347	099703	ATAXIN-2 RELATED PROTE	4.11e+00
5	40	97.6	625	11 Q99053	FILAGGRIN (FRAGMENT).	4.11e+00
6	39	95.1	1307	13 Q57683	146KDA NUCLEAR PROTEIN	7.68e+00
7	38	92.7	316	2 Q83343	RIBOSE/GALACTOSE ABC T	1.42e+01
8	38	92.7	469	2 Q56436	S-LAYER-LIKE PROTEIN.	1.42e+01
9	38	92.7	546	6 Q29111	SCAVENGER-RECEPTOR PRO	1.42e+01
10	38	92.7	682	5 Q22537	SIMILARITY TO COLLAGEN	1.42e+01
11	38	92.7	804	6 Q29113	SCAVENGER-RECEPTOR PRO	1.42e+01
12	38	92.7	1272	13 Q90924	NEUROFASCIN PRECURSOR	1.42e+01
13	38	92.7	1280	13 Q90933	NEURON-GLIA CELL ADHES	1.42e+01
14	38	92.7	1369	13 Q42414	NEUROFASCIN PRECURSOR.	1.42e+01
15	37	90.2	356	7 Q30227	MHC CLASS I AOTR-G*02	2.59e+01
16	37	90.2	511	14 Q91332	NUCLEAR ANTIGEN EBNA-1	2.59e+01
17	37	90.2	632	2 Q85869	GROUP II INTRON-ASSOCIA	2.59e+01
18	37	90.2	1095	4 Q60300	KIAA0553 PROTEIN (FRAG	2.59e+01
19	37	90.2	1190	11 P97573	INOSITOL POLYPHOSPHATE	2.59e+01
20	37	90.2	1191	11 Q61181	INOSITOL POLYPHOSPHATE	2.59e+01

21	36	87.8	95	10	Q40957	TYPE 1 LIGHT-HARVESTIN	4.67e+01
22	36	87.8	123	5	Q18672	HYPOTHETICAL PROTEIN C	4.67e+01
23	36	87.8	138	14	Q90277	REV PROTEIN.	4.67e+01
24	36	87.8	235	1	P71164	ASPARTATE RACEMASE.	4.67e+01
25	36	87.8	250	11	Q61571	FILAGGRIN (FRAGMENT).	4.67e+01
26	36	87.8	255	11	Q61570	FILAGGRIN (FRAGMENT).	4.67e+01
27	36	87.8	339	5	Q18218	CODED FOR BY C-ELEGAN	4.67e+01
28	36	87.8	511	2	Q24819	3-KETOSTEROID-DELTA1-D	4.67e+01
29	36	87.8	568	2	Q44106	MAJOR SURFACE PROTEIN	4.67e+01
30	36	87.8	699	10	Q64525	YUP812R.12 PROTEIN.	4.67e+01
31	36	87.8	1240	14	P89453	DNA POLYMERASE (EC 2.7	4.67e+01
32	36	87.8	3766	5	Q17551	SIMILAR TO REGULATOR O	4.67e+01
33	35	85.4	157	2	Q04915	OFR904 PROTEIN	8.32e+01
34	35	85.4	304	2	P96903	HYPOTHETICAL 31.4 KD P	8.32e+01
35	35	85.4	335	11	Q08283	HYPOTHETICAL ALPHA CHAIN	8.32e+01
36	35	85.4	367	3	P78852	FISSION YEAST (FRAGMEN	8.32e+01
37	35	85.4	541	11	P70430	ENABLED HOMOLOG (MENA	8.32e+01
38	35	85.4	551	10	Q81469	T15F16.13 PROTEIN.	8.32e+01
39	35	85.4	763	3	Q60013	DNA TOPOISOMERASE I.	8.32e+01
40	35	85.4	802	11	P70433	ENABLED HOMOLOG (NEURA	8.32e+01
41	35	85.4	1068	11	Q54826	MAF10.	8.32e+01
42	35	85.4	1083	5	Q26423	FACTOR C.	8.32e+01
43	35	85.4	1201	5	Q18393	MUSCLE MYOSIN HEAVY CH	8.32e+01
44	35	85.4	1276	11	P97260	SRESP CLEAVAGE ACTIVAT	8.32e+01
45	35	85.4	1920	6	Q29519	LACTASE-PHLORIZIN HYDR	8.32e+01

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT: 1095 AA.
ID	Q99458		
AC	Q99458;		
DT	01-MAY-1997 (TREMBLREL. 03, CREATED)		
DT	01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)		
DT	01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)		
DE	NOTCH4 (FRAGMENT).		
GN	NOTCH4.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;		
OC	CATARRHINI; HOMINIDAE; HOMO.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PLACENTA;		
RX	MEDLINE; 97311416.		
RA	SUGAYA K., SASANUMA S., NOHATA J., KIMURA T., FUKAGAWA T.,		
RA	NAKAMURA Y., ANDO A., INOKO H., IKEMURA T., MITA K.;		
RT	"Gene organization of human NOTCH4 and (CTG)n polymorphism in this		
RT	human counterpart gene of mouse proto-oncogene Int3."		
RL	GENE 189:235-244(1997).		
DR	EMBL; D63395; D1010354; -.		
DR	PROSITE; PS01186; EGF_2; 5.		
DR	PFAM; PF00008; EGF; 5.		
DR	PFAM; PF00023; ank; 5.		
DR	PFAM; PF00066; notch; 2.		
KW	GLYCOPROTEIN.		
FT	NON_TER 1		
SQ	SEQUENCE 1095 AA; 114807 MW; 598EA191 CRC32;		
Query Match 100.0%; Score 41; DB 4; Length 1095;			
Best Local Similarity 100.0%; Pred.No. 2.18e+00;			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	547 GRGDSP 552		
QY	1 GRGDSP 6		
RESULT	2	PRELIMINARY;	PRT: 2478 AA.
ID	Q93406		
AC	Q93406;		
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)		
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)		

DE FIBRONECTIN.  
GN ZFN.  
OS BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANTO).  
RT EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;  
OC TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;  
OC CYPRINIDAE; RASBORINAE; DANIO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA ZHAO Q., COLLODI P.;  
RT "Characterization and expression of zebrafish fibronectin."  
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF081128; G3420846; -;  
DR PROSITE: PS00223; FIBRONECTIN\_2; 2;  
SQ SEQUENCE 2478 AA; 271652 MW; 1991DF70 CRC32;  
Query Match 100.0%; Score 41; DB 13; Length 2478;  
Best Local Similarity 100.0%; Pred. No. 2.18e+00;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1613 GRGDSF 1618  
QY 1 GRGDSF 6  
|||||  
RESULT 3 PRELIMINARY; PRT; 95 AA.  
ID Q50799;  
AC Q50799;  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)  
DE COBALT TRANSPORT PROTEIN CBIN.  
GN CBIN.  
OS METHANOBACTERIUM THERMOAUTOTROPHICUM (STRAIN MARBURG).  
OC ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;  
OC METHANOBACTERIUM.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA EBERHARDT S., KORN S., LOTTSPEICH F., BACHER A.;  
RL BACTERIOL. 179:2938-2943(1997).  
CC -!- FUNCTION: MAY BE INVOLVED WITH COBALT TRANSPORT IN ASSOCIATION  
WITH COBALAMIN BIOSYNTHESIS.  
CC -!- PATHWAY: COBALAMIN BIOSYNTHESIS.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
DR EMBL: X94292; E237183; -;  
KW COBALAMIN BIOSYNTHESIS; TRANSPORT; COBALT TRANSPORT; TRANSMEMBRANE.  
FT TRANSMEM 7 27 POTENTIAL.  
FT TRANSMEM 67 87 POTENTIAL.  
SQ SEQUENCE 95 AA; 10254 MW; 81CE9869 CRC32;  
Query Match 97.8%; Score 40; DB 1; Length 95;  
Best Local Similarity 83.3%; Pred. No. 4.11e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 89 GRGESP 94  
QY 1 GRGDSF 6  
|||||  
RESULT 4 PRELIMINARY; PRT; 347 AA.  
ID Q99703;  
AC Q99703;  
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)  
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE ATAXIN-2 RELATED PROTEIN (FRAGMENT).  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;  
OC CATARRHINI; HOMINIDAE; HOMO.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 97051920.  
RA PULST S.M., NECHIPORUK A., NECHIPORUK T., GISPERT S., CHEN X.N.,  
RA LOPES-CENDES I., PEARLMAN S., STARKMAN S., OROZCO-DIAZ G., LUNKES A.,  
RA DEJONG P., ROULEAU G.A., AUBURGER G., KORENBERG J.R., FIGUEROA C.,  
RA SAHBA S.;  
RT "Moderate expansion of a normally biallelic trinucleotide repeat in  
spino cerebellar ataxia type 2.";  
RL NAT. GENET. 14:269-276(1996).  
DR EMBL: U70671; G1679686; -;  
FT NON\_TER 1 1  
SQ SEQUENCE 347 AA; 37805 MW; 9BD963F2 CRC32;  
Query Match 97.6%; Score 40; DB 4; Length 347;  
Best Local Similarity 83.3%; Pred. No. 4.11e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 283 GRGESP 288  
QY 1 GRGDSF 6  
|||||  
RESULT 5 PRELIMINARY; PRT; 625 AA.  
ID Q99053;  
AC Q99053;  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE FILAGRIN (FRAGMENT).  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;  
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-LIVER;  
RX MEDLINE: 90274870.  
RA HAYDOCK P.V., DALE B.A.;  
RT "Filaggrin, an intermediate filament-associated protein: structural  
and functional implications from the sequence of a cDNA from rat.";  
RL DNA CELL BIOL. 9:251-261(1990).  
CC -!- FUNCTION: FILAGRIN AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND  
PROMOTES DISULFIDE-BOND FORMATION AMONGST THE INTERMEDIATE  
FILAMENTS DURING TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.  
CC -!- FILAGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE, HIGHLY  
PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF 380 AA,  
WHICH ARE SEPARATED BY "LINKERS" OF 26 AA.  
CC THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.  
CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &  
PROTEOLYTICALLY CLEAVED.  
CC -!- TISSUE SPECIFICITY: EPIDERMIS, PALATE AND FORESTOMACH.  
DR EMBL: M21759; G204144; -;  
DR PIR: A34615; A34615  
KW DEVELOPMENTAL PROTEIN; PHOSPHORYLATION; POLYPROTEIN.  
FT NON\_TER 1 1  
SQ SEQUENCE 625 AA; 65957 MW; 6CD02B43 CRC32;  
Query Match 97.6%; Score 40; DB 11; Length 625;  
Best Local Similarity 83.3%; Pred. No. 4.11e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 126 GRGESP 131  
QY 1 GRGDSF 6  
|||||  
RESULT 6 PRELIMINARY; PRT; 1307 AA.  
ID O57683;  
AC O57683;  
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE 146KDA NUCLEAR PROTEIN.  
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;  
OC MESOBATRACHIA; PIPOIDEA; PIPOIDAE; XENOPODINAE; XENOPUS.  
RN [1]  
RP SEQUENCE FROM N.A.

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RA SCHMIDT-ZACHMANN M.S., KNECHT S., KRAEMER A.;
RL MOL. BIOL. CELL 9:143-160(1998).
DR EMBL; Y08997; E291018; -.
KW NUCLEAR PROTEIN.
SQ SEQUENCE 1307 AA; 146213 MW; F9E016BD CRC32;

Query Match
Best Local Similarity 95.1%; Score 39; DB 13; Length 1307;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 272 GRGDP 277
   ||||:|
QY 1 GRGDS 6

RESULT 7
ID O83343 PRELIMINARY; PRT; 316 AA.
AC O83343;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE RIBOSE/GALACTOSE ABC TRANSPORTER, PERMEASE PROTEIN (RBSC-2).
GN TP0323.
OS TREPONEMA PALLIDUM.
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHAKHAI L., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete Genome Sequence of Treponema pallidum, the Syphilis
RT Spirochete.";
RN SCIENCE 281:375-388(1998).
[2]
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHAKHAI L., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AE001212; G3322600; -.
SQ SEQUENCE 316 AA; 33824 MW; CE7DB8A0 CRC32;

Query Match
Best Local Similarity 92.7%; Score 38; DB 2; Length 316;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 298 GRGEAP 303
   ||||:|
QY 1 GRGDS 6

RESULT 8
ID Q56436 PRELIMINARY; PRT; 469 AA.
AC Q56436;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE S-LAYER-LIKE PROTEIN.
GN SLP.
OS THERMUS AQUATICUS (SUBSP. THERMOPHILUS).
OC BACTERIA; THERMUS/DEINOCOCCUS GROUP; THERMUS GROUP; THERMUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HB8;

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RA OLABARRIA G., FERNANDEZ-HERRERO L.A., CARRASCOSA J.L., BERENGUER J.;
RL J. BACTERIOL. 178:357-365(1995).
DR EMBL; X90369; G993026; -.
KW S-LAYER.
SQ SEQUENCE 469 AA; 52131 MW; 87F62633 CRC32;

Query Match
Best Local Similarity 92.7%; Score 38; DB 2; Length 469;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 178 GRGEAP 183
   ||||:|
QY 1 GRGDS 6

RESULT 9
ID O29111 PRELIMINARY; PRT; 546 AA.
AC O29111;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SCAVENGER-RECEPTOR PROTEIN PRECURSOR (FRAGMENT).
GN WCL.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SLAB/B;
RX MEDLINE; 97364683.
RA KANAN J.H.C., NAYEM N., BINNS R.M., CHAIN B.M.;
RT "Mechanisms for variability in a member of the scavenger-receptor
RT cysteine-rich superfamily.";
RL IMMUNOGENETICS 46:276-282(1997).
DR EMBL; X99334; E254903; -.
DR PFAM; PF00530; SRCR; 5.
KW SIGNAL.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 >546 SCAVENGER-RECEPTOR PROTEIN.
FT NON TER 546 546
SQ SEQUENCE 546 AA; 59112 MW; F98A0F1F CRC32;

Query Match
Best Local Similarity 92.7%; Score 38; DB 6; Length 546;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 83 GRGDS 88
   ||||:|
QY 1 GRGDS 6

RESULT 10
ID Q22537 PRELIMINARY; PRT; 682 AA.
AC Q22537;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SIMILARITY TO COLLAGEN.
GN T1H7.1
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

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RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans";  
 RL NATURE 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA FAVELLO A.;  
 RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: U42841; G1125784;  
 SQ SEQUENCE 682 AA; 72150 MW; 0EF72EE3 CRC32;

Query Match 92.7%; Score 38; DB 5; Length 682;  
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 228 GRGDGP 233  
 |||||  
 QY 1 GRGDSP 6

RESULT 11  
 ID Q29113 PRELIMINARY; PRT; 804 AA.  
 AC Q29113;  
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)  
 DE SCVENGER-RECEPTOR PROTEIN PRECURSOR.  
 GN WCI  
 OS SUS SCROFA (PIG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SLAB/B;  
 RX MEDLINE; 97364683.  
 RA KANAN J.H.C., NAYEM N., BINNS R.M., CHAIN B.M.;  
 RT "Mechanisms for variability in a member of the scavenger-receptor  
 RT cysteine-rich superfamily";  
 RL IMMUNOGENETICS 46:276-282(1997).  
 DR EMBL: X99336; E254904;  
 DR PFAM; PF00530; SRCR; 5.  
 KW SIGNAL.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 >804 SCAVENGER-RECEPTOR PROTEIN.  
 SQ SEQUENCE 804 AA; 86627 MW; 64125250 CRC32;

Query Match 92.7%; Score 38; DB 6; Length 804;  
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 83 GRGDGP 88  
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 QY 1 GRGDSP 6

RESULT 12  
 ID Q90924 PRELIMINARY; PRT; 1272 AA.  
 AC Q90924;  
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)  
 DE NEUROFASCIN PRECURSOR.  
 OS GALLUS GALLUS (CHICKEN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;  
 OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 92317154.  
 RA VOLKMER H., HASSEL B., WOLFF J.M., FRANK R., RATHJEN F.G.;

RT "Structure of the axonal surface recognition molecule neurofascin and  
 its relationship to a neural subgroup of the immunoglobulin  
 RT superfamily";  
 RL J. CELL BIOL. 118:149-161(1992).  
 DR EMBL: X65224; G63660;  
 DR PFAM; PF00041; fn3; 4.  
 DR PFAM; PF00047; ig; 6.  
 KW SIGNAL.  
 FT SIGNAL 1 25 POTENTIAL.  
 SQ SEQUENCE 1272 AA; 142242 MW; 02CCB48F CRC32;

Query Match 92.7%; Score 38; DB 13; Length 1272;  
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 928 GRGDGP 933  
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 QY 1 GRGDSP 6

RESULT 13  
 ID Q90933 PRELIMINARY; PRT; 1280 AA.  
 AC Q90933;  
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)  
 DE NEURON-GLIA CELL ADHESION MOLECULE (NG-CAM) PRECURSOR (NG-CAM).  
 OS GALLUS GALLUS (CHICKEN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;  
 OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WHITE LEHORN; TISSUE-BRAIN;  
 RX MEDLINE; 97133428.  
 RA BUCHSTALLER A., KUNZ S., BERGER P., KUNZ B., ZIEGLER U., RADER C.,  
 RA SONDEREGGER P.;  
 RT "Cell adhesion molecules NgCAM and axonin-1 form heterodimers in the  
 RT neuronal membrane and cooperate in neurite outgrowth promotion";  
 RL J. CELL BIOL. 135:1593-1607(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WHITE LEHORN; TISSUE-BRAIN;  
 RX MEDLINE; 91154306.  
 RA BURGOON M.P., GRUMET M., MAURO V., EDELMAN G.M., CUNNINGHAM B.A.;  
 RT "Structure of the chicken neuron-glia cell adhesion molecule, Ng-CAM:  
 RT origin of the polypeptides and relation to the Ig superfamily";  
 RL J. CELL BIOL. 112:1017-1029(1991).  
 DR EMBL: Z75013; E256949;  
 DR PFAM; PF00041; fn3; 5.  
 DR PFAM; PF00047; ig; 6.  
 KW SIGNAL.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 1280 NEURON-GLIA CELL ADHESION MOLECULE  
 (NG-CAM).  
 SQ SEQUENCE 1280 AA; 138432 MW; A72DEE34 CRC32;

Query Match 92.7%; Score 38; DB 13; Length 1280;  
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 919 GRGDGP 924  
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 QY 1 GRGDSP 6

RESULT 14  
 ID O42414 PRELIMINARY; PRT; 1369 AA.  
 AC O42414;  
 DT 01-JAN-1998 (TREMELREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)  
 DE NEUROFASCIN PRECURSOR.  
 OS GALLUS GALLUS (CHICKEN).

Search completed: Thu Dec 23 10:09:11 1999  
Job time : 40 secs.

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OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC  NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=LIVER;
RA  HASSEL B., RATHJEN F.G., VOLKMER H.;
RA  MEDLINE; 98019255.
RT  "Organization of the neurofascin gene and analysis of developmentally
RL  regulated alternative splicing.";
RL  J. BIOL. CHEM. 272:28742-28749(1997).
DR  EMBL; Y14343; E331970; JOINED.
DR  EMBL; Y14344; E331970; JOINED.
DR  EMBL; Y14345; E331970; JOINED.
DR  EMBL; Y14346; E331970; JOINED.
DR  EMBL; Y14347; E331970; JOINED.
DR  EMBL; Y14348; E331970; JOINED.
DR  EMBL; Y14341; E331970; -
DR  EMBL; Y14342; E331970; JOINED.
DR  EMBL; Y14349; E331970; JOINED.
DR  EMBL; Y14353; E331970; JOINED.
DR  EMBL; Y14354; E331970; JOINED.
DR  EMBL; Y14350; E331970; JOINED.
DR  EMBL; Y14351; E331970; JOINED.
DR  EMBL; Y14352; E331970; JOINED.
DR  PFAM; PF00041; fn3; 5.
DR  PFAM; PF00047; i9; 6.
KW  SIGNAL.
FT  SIGNAL
FT  CHAIN
SQ  SEQUENCE 1369 AA; 152954 MW; F926E6B4 CRC32;

Query Match          92.7%; Score 38; DB 13; Length 1369;
Best Local Similarity 83.3%; Pred. No. 1.42e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db  928 GRGDGP 933
Qy  1 GRGDSP 6
      |||||:1

RESULT 15
ID  Q30227      PRELIMINARY;      PRT;      356 AA.
AC  Q30227;
DT  01-NOV-1996 (TREMBLREL. 01, CREATED)
DT  01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT  01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE  MHC CLASS I AOTR-G*02 (FRAGMENT).
GN  AOTR-G.
OS  AOTUS TRIVIRGATUS (NIGHT MONKEY) (DOUROUCOULI).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC  PLATYRRHINI; CEBIDAE; AOTINAE; AOTUS.
RN  [1]
RP  SEQUENCE FROM N.A.
RA  CADAVIN L.F., SHUFFLEBOTHAM C., RUIZ F.J., YEAGER M., HUGHES A.L.,
RA  WATKINS D.I.;
RT  "Evolutionary instability of the major histocompatibility complex
RL  class I loci in New World primates.";
RL  PROC. NATL. ACAD. SCI. U.S.A. 94:14536-14541(1997).
DR  EMBL; U59645; G1389917; -
DR  PFAM; PF00047; i9; 1.
DR  PFAM; PF00129; MHC_I; 1.
DR  KW MHC.
FT  NON_TER
FT  SEQUENCE 356 AA; 39726 MW; B3A2E8B0 CRC32;

Query Match          90.2%; Score 37; DB 7; Length 356;
Best Local Similarity 66.7%; Pred. No. 2.59e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db  32 GRGEPP 37
Qy  1 GRGDSP 6
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